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42

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Morris Reichlin and Eugen Koren
- (ii) TITLE OF INVENTION: METHOD FOR TREATMENT OF SLE

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

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1201 West Peachtree Street
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- (D) STATE: Georgia
- (E) COUNTRY: USA
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(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/800,682
- (B) FILING DATE: 14-FEB-1997
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 60/011,867
- (B) FILING DATE: 15-FEB-1996
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

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(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1

GGTGAAGAAG GAGTTGTGCC AGCACGTGAG TACTCAGACG ATCGTAACAT CAACCTGGCA	60
GACGAATTAA AAATTGGTGA TACCATTGAA GCAGTTGTCA TTTCTAACGT AACAAAGCGAC	120
AAGGAAGGCG TCAGTTACTT GTTGTCAAAG AAGCGTTTGG ATGCGCGCAA GGCATGGGAA	180
AACTTGAGCT TTGCTGAAGG TGACACAGTT GATGCCAAGG TTATCAACGC TGTTCTGGGT	240
GGTTTGATTG TTGATGTTAA CGGCGTACGT GGTTTCGTAC CAGCATCAAT GGTTCAGAA	300

CGTTTCGTTT CTGATTGAA CCAATTCAAG AATAAGGATA TTAAAGCACA AGTTATCGAA 360
ATTGACCCTG CTAATGCACG TTTGATTTTG TCACGTAAGG CTGTTGCTGC ACAAGAACGC 420
GCTGCACGAT TGGCTGAAGT ATTTAGCAAG TTGTCAGTTC GTGAAGTTGT TGAAGGAACT 480
GTTGCCCCGT TGACAGACTT CGGCGCATTC GTTGACTTGG GTGGTGTTGA TGGTTTGTTT 540
CACGTATCAG AAATCTCACA CGATCGTGTG AAGAACCCCG CCGATGTATT GACAAAGGGT 600
GACAAGGTTG ATGTTAAGAT CTTGGCATTG GACACTGAAA AGGGTCGTAT CTCATTGTCA 660
ATCAAAGCAA CACAACGTGG ACCTTGGGAC GAAGCTGCAG ATCAAATCGC TGCAGGTTCA 720
GTGCTTGAAG GTACTGTTAA GCGTGTGAAG GACTTTGGTG CCTTTGTTGA AATTTTGCCT 780
GGTATCGAAG GTCTTGTGCA CGTGTACAAA ATTTCAAACA AGCGTATTGA AAACCCATCA 840
GAAGTTTTGA AGTCTGGTGA CAAGGTACAA GTGAAGGTAT TGGACATTAA GCCAGCCGAA 900
GAACGTATTT CATTGTCAAT GAAGGCTTTG GAAGAAAAGC CAGAACGTGA AGATCGTCGT 960
GGTAACGATG GTTCAGCTTC ACGTGCTGAT ATCGCTGCTT ACAAGCAACA AGATGACTCA 1020
GCCGCAACAT TGGGTGACAT CTTTGGTGAT AAGTTGTAAG AGGCATCAAC ATAAAAGAGC 1080
TGGTTCGCCA GTTCTTTTAT TTTTGAAGAA AAATTGAGTG GGCATTAGTG GGCGCTCACG 1140
GTATGAAAAA GGAGGTGCGA TTATGGCAGC ACCAGTAGTA GCCATTGTTG GCGACCAAAC 1200
GTCGGAAAAT CGACTATCTT TAACCGGATG GCCGGAGAAC GTATTGCAAT TGTTGAAGAT 1260
CAACCAGGGG TAACACGCGA TCGTTTGTAC GCGCCAGCCG AATGTTGAA TTAT 1314

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2

Gly Glu Glu Gly Val Val Pro Ala Arg Glu Tyr Ser Asp Asp Arg Asn
1 5 10 15
Ile Asn Leu Ala Asp Glu Leu Lys Ile Gly Asp Thr Ile Glu Ala Val
20 25 30
Val Ile Ser Asn Val Thr Ser Asp Lys Glu Gly Val Ser Tyr Leu Leu
35 40 45
Ser Lys Lys Arg Leu Asp Ala Arg Lys Ala Trp Glu Asn Leu Ser Phe
50 55 60
Ala Glu Gly Asp Thr Val Asp Ala Lys Val Ile Asn Ala Val Arg Gly
65 70 75 80
Gly Leu Ile Val Asp Val Asn Gly Val Arg Gly Phe Val Pro Ala Ser
85 90 95

Met Val Ala Glu Arg Phe Val Ser Asp Leu Asn Gln Phe Lys Asn Lys
 100 105 110
 Asp Ile Lys Ala Gln Val Ile Glu Ile Asp Pro Ala Asn Ala Arg Leu
 115 120 125
 Ile Leu Ser Arg Lys Ala Val Ala Ala Gln Glu Arg Ala Ala Gln Leu
 130 135 140
 Ala Glu Val Phe Ser Lys Leu Ser Val Gly Glu Val Val Glu Gly Thr
 145 150 155 160
 Val Ala Arg Leu Thr Asp Phe Gly Ala Phe Val Asp Leu Gly Gly Val
 165 170 175
 Asp Gly Leu Val His Val Ser Glu Ile Ser His Asp Arg Val Lys Asn
 180 185 190
 Pro Ala Asp Val Leu Thr Lys Gly Asp Lys Val Asp Val Lys Ile Leu
 195 200 205
 Ala Leu Asp Thr Glu Lys Gly Arg Ile Ser Leu Ser Ile Lys Ala Thr
 210 215 220
 Gln Arg Gly Pro Trp Asp Glu Ala Ala Asp Gln Ile Ala Ala Gly Ser
 225 230 235 240
 Val Leu Glu Gly Thr Val Lys Arg Val Lys Asp Phe Gly Ala Phe Val
 245 250 255
 Glu Ile Leu Pro Gly Ile Glu Gly Leu Val His Val Ser Gln Ile Ser
 260 265 270
 Asn Lys Arg Ile Glu Asn Pro Ser Glu Val Leu Lys Ser Gly Asp Lys
 275 280 285
 Val Gln Val Lys Val Leu Asp Ile Lys Pro Ala Glu Glu Arg Ile Ser
 290 295 300
 Leu Ser Met Lys Ala Leu Glu Glu Lys Pro Glu Arg Glu Asp Arg Arg
 305 310 315 320
 Gly Asn Asp Gly Ser Ala Ser Arg Ala Asp Ile Ala Ala Tyr Lys Gln
 325 330 335
 Gln Asp Asp Ser Ala Ala Thr Leu Gly Asp Ile Phe Gly Asp Lys Leu
 340 345 350

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3

Ser Phe Ala Glu Gly Asp Thr Val Asp Ala Lys Val Ile Asn Ala Val
 1 5 10 15

Arg Gly Gly Leu Ile Val Asp Val Asn Gly Val Arg Gly Phe Val Pro
 20 25 30
 Ala Ser Met Val Ala Glu Arg Phe Val Ser Asp Leu Asn Gln Phe Lys
 35 40 45
 Asn Lys Asp Ile Lys Ala Gln Val Ile Glu Ile Asp Pro Ala Asn Ala
 50 55 60
 Arg Leu Ile Leu Ser Arg Lys Ala Val Ala Ala Gln Glu Arg Ala Ala
 65 70 75 80
 Gln Leu Ala Glu Val Phe Ser Lys Leu Ser Val Gly Glu Val Val Glu
 85 90 95
 Gly Thr Val Ala Arg Leu Thr Asp Phe Gly Ala Phe Val Asp Leu Gly
 100 105 110
 Gly Val Asp Gly Leu Val His Val Ser Glu Ile Ser His Asp Arg Val
 115 120 125
 Lys Asn Pro Ala Asp Val Leu Thr Lys Gly Asp Lys Val Asp Val Lys
 130 135 140
 Ile Leu Ala Leu Asp Thr Glu Lys Gly Arg Ile Ser Leu Ser Ile Lys
 145 150 155 160
 Ala Thr Gln Arg Gly Pro Trp Asp Glu Ala Ala Asp Gln Ile Ala Ala
 165 170 175
 Gly Ser Val Leu Glu Gly Thr Val Lys Arg Val Lys Asp Phe Gly Ala
 180 185 190
 Phe Val Glu Ile Leu Pro Gly Ile Glu Gly Leu Val His Val Ser Gln
 195 200 205
 Ile Ser Asn Lys Arg Ile Glu Asn Pro Ser Glu Val Leu Lys Ser Gly
 210 215 220
 Asp Lys Val Gln Val Lys Val Leu Asp Ile Lys Pro Ala Glu Glu Arg
 225 230 235 240
 Ile Ser Leu Ser Met Lys Ala Leu Glu Glu Lys Pro Glu Arg Glu
 245 250 255

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4

Ala Tyr Glu Asp Ala Glu Thr Val Thr Gly Val Ile Asn Gly Lys Val
 1 5 10 15
 Lys Gly Gly Phe Thr Val Glu Leu Asp Gly Ile Arg Ala Phe Leu Pro
 20 25 30

Gly Ser Leu Val Asp Val Arg Pro Val Arg Asp Thr Leu His Leu Glu
 35 40 45
 Gly Lys Glu Leu Glu Phe Lys Val Ile Lys Leu Asp Gln Lys Arg Asn
 50 55 60
 Asn Val Val Val Ser Arg Arg Ala Val Ile Glu Ser Glu Asn Ser Ala
 65 70 75 80
 Glu Arg Asp Gln Leu Leu Glu Asn Leu Gln Glu Gly Met Glu Val Lys
 85 90 95
 Gly Ile Val Lys Asn Leu Thr Asp Tyr Gly Ala Phe Val Asp Leu Gly
 100 105 110
 Gly Val Asp Gly Leu Leu His Ile Thr Asp Met Ala Trp Lys Arg Val
 115 120 125
 Lys His Pro Ser Glu Ile Val Asn Val Gly Asp Glu Ile Thr Val Lys
 130 135 140
 Val Leu Lys Phe Asp Arg Glu Arg Thr Arg Val Ser Leu Gly Leu Lys
 145 150 155 160
 Gln Leu Gly Glu Asp Pro Trp Val Ala Ile Ala Lys Arg Tyr Pro Glu
 165 170 175
 Gly Thr Lys Leu Thr Gly Arg Val Thr Asn Leu Thr Asp Tyr Gly Cys
 180 185 190
 Phe Val Glu Ile Glu Glu Gly Val Glu Gly Leu Val His Val Ser Glu
 195 200 205
 Met Arg Asp Arg Val Glu Asp Ala Thr Leu Val Leu Ser Val Gly Asp
 210 215 220
 Glu Val Glu Ala Lys Phe Thr Gly Val Asp Arg Lys Asn Arg Ala Ile
 225 230 235 240
 Ser Leu Ser Val Arg Ala Lys Asp Glu Ala Asp Glu Lys Asp
 245 250

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5

Lys Phe Glu Ala Gly Glu Arg Val Glu Gly Ile Ile Phe Asn Gln Val
 1 5 10 15
 Lys Gly Gly Phe Thr Val Asp Leu Asp Gly Ala Val Ala Phe Leu Pro
 20 25 30
 Arg Ser Gln Val Asp Ile Arg Pro Ile Arg Asp Val Thr Pro Ala Asp
 35 40 45

Ala Gln Pro Ala Ala Leu Arg Asn Leu Lys Met Asp Lys Arg Arg Gly
 50 55 60

Asn Ile Val Val Ser Arg Arg Thr Val Leu Glu Glu Ser Arg Ala Glu
 65 70 75 80

Gln Arg Ser Glu Ile Val Gln Asn Leu Glu Glu Gly Gln Val Val Glu
 85 90 95

Gly Val Val Lys Asn Ile Thr Asp Tyr Gly Ala Phe Val Asp Leu Gly
 100 105 110

Gly Ile Asp Gly Leu Leu His Val Thr Asp Met Ala Trp Arg Arg Val
 115 120 125

Lys His Pro Ser Glu Ile Gln Asn Ile Gly Gln Gln Val Lys Val Gln
 130 135 140

Ile Ile Arg Ile Asn Gln Glu Thr His Arg Ile Ser Leu Gly Met Lys
 145 150 155 160

Gln Leu Glu Ser Asp Pro Trp Asp Gly Ile Gly Ala Lys Tyr Pro Val
 165 170 175

Gly Lys Lys Ile Ser Gly Thr Val Thr Asn Ile Thr Asp Tyr Gly Ala
 180 185 190

Phe Val Glu Leu Glu Pro Gly Ile Glu Gly Leu Ile His Ile Ser Glu
 195 200 205

Met Asn Arg Pro Gly Glu Gln Val Ile Glu Glu Phe Asn Lys Gly Asp
 210 215 220

Val Val Arg Ala Val Val Leu Asp Val Asp Val Asp Lys Glu Arg Ile
 225 230 235 240

Ser Leu Gly Ile Lys Gln Leu
 245

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6

Glu Thr Val Thr Gly Val Ile Asn Gly Lys Val Lys Gly Gly Phe Thr
 1 5 10 15

Val Glu Leu Asn Gly Ile Arg Ala Phe Leu Pro Gly Ser Leu Val Asp
 20 25 30

Val Arg Pro Val Arg Asp Thr Thr His Leu Glu Gly Lys Glu Leu Glu
 35 40 45

Phe Lys Val Ile Lys Leu Asp Gln Lys Arg Asn Asn Val Val Val Ser
 50 55 60
 Arg Arg Ala Val Ile Glu Ser Glu Ser Ser Ala Glu Arg Asp Gln Leu
 65 70 75 80
 Leu Glu Asn Leu Gln Glu Gly Met Glu Val Lys Gly Ile Val Lys Asn
 85 90 95
 Leu Thr Asp Tyr Gly Ala Phe Val Asp Leu Gly Gly Val Asp Gly Leu
 100 105 110
 Leu His Ile Thr Asp Met Ala Trp Lys Arg Val Lys His Pro Ser Glu
 115 120 125
 Ile Val Asn Val Gly Asp Glu Ile Thr Val Lys Val Leu Lys Phe Asp
 130 135 140
 Arg Glu Arg Thr Arg Val Ser Leu Gly Leu Lys Gln Leu Gly Glu Asp
 145 150 155 160
 Pro Trp Val Ala Ile Ala Lys Arg Tyr Pro Glu Gly Thr Lys Leu Thr
 165 170 175
 Gly Arg Val Thr Asn Leu Thr Asp Tyr Gly Cys Phe Val Glu Ile Glu
 180 185 190
 Glu Gly Val Glu Gly Leu Val His Val Ser Glu Met Lys Lys Gly Asp
 195 200 205
 Glu Ile Ala Ala Val Val Leu Gln Val Asp Ala Glu Arg Glu Arg Ile
 210 215 220
 Ser Leu Gly Val Lys Gln Leu Ala Glu Asp Pro
 225 230 235

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7

Ala Glu Asp Val Val Val Lys Gly Lys Ile Val Gly Ala Asn Lys Gly
 1 5 10 15
 Gly Val Val Ala Leu Val Glu Gly Leu Arg Gly Phe Val Pro Phe Ser
 20 25 30
 Gln Ile Ser Ser Lys Ser Ser Ala Glu Glu Leu Leu Glu Lys Glu Ile
 35 40 45
 Pro Leu Lys Phe Val Glu Val Asp Glu Glu Gln Ser Arg Leu Val Met
 50 55 60
 Ser Asn Arg Lys Ala Met Ala Asp Ser Gln Ala Met Ala Asp Ser Gln
 65 70 75 80

Ala Gln Leu Gly Ile Gly Ser Val Val Thr Gly Thr Val Gln Ser Leu
 85 90 95

Lys Pro Tyr Gly Ala Phe Ile Asp Ile Gly Gly Ile Asn Gly Leu Leu
 100 105 110

His Val Ser Gln Ile Ser His Asp Arg Val Ser Asp Ile Ala Thr Val
 115 120 125

Leu Gln Pro Gly Asp Thr Leu Lys Val Met Ile Leu Ser His Asp Arg
 130 135 140

Glu Arg Gly Arg Val Ser Leu Ser Thr Lys Lys Leu Glu Pro Thr Pro
 145 150 155 160

Gly Asp

- (2) INFORMATION FOR SEQ ID NO:8:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu Gly Thr Val
 1

- (2) INFORMATION FOR SEQ ID NO:9:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9

Asp Phe Gly Ala Phe Val
 1 5

- (2) INFORMATION FOR SEQ ID NO:10:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (iv) ANTI-SENSE: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10

Gly Leu Val His Val Ser
 1 5

- (2) INFORMATION FOR SEQ ID NO:11:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11

Gly Asp Lys Val

1

- (2) INFORMATION FOR SEQ ID NO:12:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

Arg Ile Ser Leu Ser

1

5